GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 27, 2003, 11:12:13 ; Search time 289 Seconds
(without alignments)
1.234 Million cell updates/sec

Title: al512306
Perfect score: 133984
Sequence: 1 GCAGGCCAAGTTCTTGGGCA.....AAAACAAAATGGCTGAATTC 133984

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1331 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : mayes.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	720.4	0.5	1331	1	US-09-830224B-2	Sequence 2, Appli
	2	37.4	0.0	1331	1	US-09-830224B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-830224B-2/c
; Sequence 2, Application US/09830244B
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: LYSINE-RICH STATHERIN PROTEIN
; FILE REFERENCE: PF-0620 USN
; CURRENT APPLICATION NUMBER: US/09/830,244B
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/US99/24046
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/155,209
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2820214CB1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1242
; OTHER INFORMATION: a, t, c, g, or other
US-09-830224B-2

Query Match 0.5%; Score 720.4; DB 1; Length 1331;
Best Local Similarity 61.1%; Pred. No. 0;
Matches 1074; Conservative 0; Mismatches 16; Indels 668; Gaps 1;

```
Qy      90881 TAAAGATACTGTAGTTACAAGGGCTGATAAGGGTCTTTGGTATAAAAGCAATATCCAGAA 90940
              || ||   ||| |  | ||||||||||| ||||||||||||||||||||||||||||
Db       1090 TATAGTGGTTGTTCTGGAACTGGCTGATAAGGCTCTTTGGTATAAAAGCAATATCCAGAA 1031

Qy      90941 ATAAGATAATTAACTTTGGAACTAAGGGGATATAAATGACACAGTAAAGGTGGAAGGGTT 91000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 ATAAGATAATTAACTTTGGAACTAAGGGGATATAAATGACACAGTAAAGGTGGAAGGGTT 971

Qy      91001 TTTTTTTCTTAAGGGAGACCAGAGTTTTATTATTACTCAAATCAGTCTCCCAAAAAGTTA 91060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 TTTTTTTCTTAAGGGAGACCAGAGTTTTATTATTACTCAAATCAGTCTCCCAAAAAGTTA 911

Qy      91061 CTTTAAAATGCTGTTTTCTTCCCACTTTATGAAACCACATTTGCTACTGTTGACAGGGGA 91120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CTTTAAAATGCTGTTTTCTTCCCACTTTATGAAACCACATTTGCTACTGTTGACAGGGGA 851

Qy      91121 CTATCTGATCAGAAATATTTGTCTGTTGACATCAGTACTTAACTGTTTAAAAAAAAAAAC 91180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTATCTGATCAGAAATATTTGTCTGTTGACATCAGTACTTAACTGTTTAAAAAAAAAAAC 791

Qy      91181 AGTGCCTTCAGATAAGAAATTAGGGGCTCTAATAAGATGTTATAATGATAAATGTCCTTT 91240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 AGTGCCTTCAGATAAGAAATTAGGGGCTCTAATAAGATGTTATAATGATAAATGTCCTTT 731

Qy      91241 TTTTTGAGACAGAGTCTCTGTCACCCAGGTGGGAGCGCAGTGGTGCAGTCTCGGCTCACT 91300
              ||||||||||||||||||||||
Db        730 TTTTTGAGACAGAGTCTCTGTC---------------------------------------- 709

Qy      91301 GCAACCTCCACCTCCCAGGTTCAAGCGATTCTCCTGTCTCAACCTGCCAAGTAGCTGGGA 91360
Db        708 ---------------------------------------------------------- 709

Qy      91361 CTACAGGTGCACGCCACCACGACCGGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTC 91420
Db        708 ---------------------------------------------------------- 709

Qy      91421 ACCATACTGGTCAGACTGGTCTCGAACTCCTGAGCTCAGGCAATCCACCCACCTCGGCCT 91480
Db        708 ---------------------------------------------------------- 709

Qy      91481 CCCAAAGTGCTGGGATTACAGGCGTAAGCCACCGCCCCTAGCCTAATATCAATCTTCGAT 91540
Db        708 ---------------------------------------------------------- 709

Qy      91541 AAAGCATTTGCCAAATTACAGCAACTGCTCTGAAAGAGGAATTGCTCTTCTAGCATTATT 91600
Db        708 ---------------------------------------------------------- 709

Qy      91601 TGACCCTTTTTAGGTATCCTTGACCCTCTTTACCTTAAGAAATGGAGAGTTCCGGCCGGG 91660
Db        708 ---------------------------------------------------------- 709

Qy      91661 CGCGGTGGCTCACGCCTGTAATCCCAGTACTTTGGGAGGCTGAGGTGGGCAGATCACGAG 91720
Db        708 ---------------------------------------------------------- 709

Qy      91721 GTCAGGAGATCAAGACCATCCTGGCTAAGACGGTGAAACCCCGTCTCCAATAAAAATACA 91780
Db        708 ---------------------------------------------------------- 709

Qy      91781 AAAATTAGCCAGGCGTGGTGGCGGGCGCCTATAGTCCCAGCTACTAGGGAGGCTGAGGCA 91840
Db        708 ---------------------------------------------------------- 709
```

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Qy      91841 GGAGAATGGGGTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCACTGCAC 91900
Db        708 ------------------------------------------------------------ 709
Qy      91901 TCCAGCCGGGGCGACAGAGAGAGACTCCGTCTAAAAAAAAAAAAAAAGAAATGGAGAGTT 91960
                                        ||||||| |||| ||||||||||||||||
Db        708 ----------------------------TTAAAAAACAAAACAAAGAAATGGAGAGTT 679
Qy      91961 CTACTAACTGTCCTGTGCTCCCAGAGGGGATTCAATGAGGATCGTAAGAAGGAAAACAAC 92020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 CTACTAACTGTCCTGTGCTCCCAGAGGGGATTCAATGAGGATCGTAAGAAGGAAAACAAC 619
Qy      92021 CTGCAGGGGAAGCAGCATCTTGGATTTCAGATAAAGTACCAAAAAATATTAGCTATCTCT 92080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CTGCAGGGGAAGCAGCATCTTGGATTTCAGATAAAGTACCAAAAAATATTAGCTATCTCT 559
Qy      92081 TTCTGCAGACATGCCTCTTTCTCTGTTAACACTTTCAGTCATTCAAAAGGCTATTGGTAG 92140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 TTCTGCAGACATGCCTCTTTCTCTGTTAACACTTTCAGTCATTCAAAAGGCTATTGGTAG 499
Qy      92141 AGGTGCAGCAAATCCAAGTGTAGATTTACTGTAACAGTTTATTTAACTATGCTGTATTCA 92200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AGGTGCAGCAAATCCAAGTGTAGATTTACTGTAACAGTTTATTTAACTATGCTGTATTCA 439
Qy      92201 CCAATAACGGCATTACCAATAATGGCATTAGTGCACATCAAAAGATCTGAAAATGCTAAT 92260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CCAATAACGGCATTACCAATAATGGCATTAGTGCACATCAAAAGATCTGAAAATGCTAAT 379
Qy      92261 GGGACATTTCCCACAAAAGGAAAGAAATCCAATGGCTCCTATAAAGGGAGAATATAGCAA 92320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GGGACATTTCCCACAAAAGGAAAGAAATCCAATGGCTCCTATAAAGGGAGAATATAGCAA 319
Qy      92321 TGGCAAGCAGAATGAAAATTTCTGTCAAAAGAAAGTACTTCTCAAAGCAATCAGGAAAAA 92380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TGGCAAGCAGAATGAAAATTTCTGTCAAAAGAAAGTACTTCTCAAAGCAATCAGGAAAAA 259
Qy      92381 CTGTTCCCAAATTAGGCCTGGGGAGCCACATTAGCCACTATCTCAGATACTGATTATTTT 92440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CTGTTCCCAAATTAGGCCTGGGGAGCCACATTAGCCACTATCTCAGATACTGATTATTTT 199
Qy      92441 GTTTAGCCTTAGGGGCCTCAATATTCCCCCTCATCTGCTAAACTTCAACTTGTTTACTCA 92500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GTTTAGCCTTAGGGGCCTCAATATTCCCCCTCATCTGCTAAACTTCAACTTGTTTACTCA 139
Qy      92501 CAAGTCTGATAAATTCCAGCCAAGTAACCTTAACATTCCCTATGGCAGTGCAAAATTCCA 92560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 CAAGTCTGATAAATTCCAGCCAAGTAACCTTAACATTCCCTATGGCAGTGCAAAATTCCA 79
Qy      92561 GACATTTGTAAACACTGTAAATTTCACGTTTGGTACATGAGACAGCTTACCGGTTCATCT 92620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GACATTTGTAAACACTGTAAATTTCACGTTTGGTACATGAGACAGCTTACCGGTTCATCT 19
Qy      92621 TTGATTCTAAAAACATAG 92638
              ||||||||||||||||||
Db         18 TTGATTCTAAAAACATAG 1
```

RESULT 2
US-09-830224B-2
; Sequence 2, Application US/09830244B
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: LYSINE-RICH STATHERIN PROTEIN
; FILE REFERENCE: PF-0620 USN
; CURRENT APPLICATION NUMBER: US/09/830,244B
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/US99/24046
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/155,209
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2820214CB1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1242
; OTHER INFORMATION: a, t, c, g, or other
US-09-830224B-2

Query Match 0.0%; Score 37.4; DB 1; Length 1331;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy      70292 AATGCTTGGGGAGACTAATTTGAGTAATAATAAAACTCCGGTCTCCC 70338
              ||   || |||||||| |||||||||||||||||||| ||||||||
Db        912 AACTTTTTGGGGAGACTGATTTGAGTAATAATAAAACTCTGGTCTCCC 958
```

Search completed: June 27, 2003, 11:17:21
Job time : 301 secs

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 27, 2003, 12:14:57 ; Search time 13.5 Seconds
(without alignments)
1.886 Million cell updates/sec

Title: al512306
Perfect score: 238409
Sequence: 1 GCAGGCCAAGTTCTTGGGCA.....AAAACAAAATGGCTGAATTC 133984

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 95 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=soft -Q=al512306.seq -DB=mayes.pep -SUFFIX=pto -OUT=mayesaa -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : mayes.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	349	0.1	95	1	US-09-830244B-1	Sequence 1, Appli
2	58.5	0.0	95	1	US-09-830244B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-830244B-1
; Sequence 1, Application US/09830244B
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: LYSINE-RICH STATHERIN PROTEIN
; FILE REFERENCE: PF-0620 USN
; CURRENT APPLICATION NUMBER: US/09/830,244B
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/US99/24046
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/155,209
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2820214CD1
US-09-830244B-1

Alignment Scores:

Pred. No.:	0	Length:	95
Score:	349.00	Matches:	65
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.48%	Mismatches:	0
Query Match:	0.15%	Indels:	0
DB:	1	Gaps:	0

al512306 (1-133984) x US-09-830244B-1 (1-95)

```
Qy      91100 ATGTGGTTTCATAAAGTGGGAAGAAAACAGCATTTTAAAGTAACTTTTTGGGAGACTGAT 91041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetTrpPheHisLysValGlyArgLysGlnHisPheLysValThrPheTrpGluThrAsp 20

Qy      91040 TTGAGTAATAATAAAACTCTGGTCTCCCTTAAGAAAAAAAAACCCTTCCACCTTTACTGT 90981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 LeuSerAsnAsnLysThrLeuValSerLeuLysLysLysLysProPheHisLeuTyrCys 40

Qy      90980 GTCATTTATATCCCCTTAGTTCCAAAGTTAATTATCTTATTTCTGGATATTGCTTTTATA 90921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValIleTyrIleProLeuValProLysLeuIleIleLeuPheLeuAspIleAlaPheIle 60

Qy      90920 CCAAAGACCCTTATCAGC 90903
              ||||||:::|||||||||
Db         61 ProLysSerLeuIleSer 66
```

RESULT 2
US-09-830244B-1
; Sequence 1, Application US/09830244B
; GENERAL INFORMATION:
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: LYSINE-RICH STATHERIN PROTEIN
; FILE REFERENCE: PF-0620 USN
; CURRENT APPLICATION NUMBER: US/09/830,244B
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/US99/24046
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/155,209
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2820214CD1
US-09-830244B-1

Alignment Scores:

Pred. No.:	0	Length:	95
Score:	58.50	Matches:	20
Percent Similarity:	47.54%	Conservative:	9
Best Local Similarity:	32.79%	Mismatches:	24
Query Match:	0.02%	Indels:	8
DB:	1	Gaps:	2

al512306 (1-133984) x US-09-830244B-1 (1-95)

```
Qy      104105 AAGAATGTTACCCTTTCAAAAGAAAAAAAACCACTTCCCTTCAAATGTGAAATTTAC--- 104161
               |||   :::         |||:::|||||||||            |||   ||||||
Db          25 LysThrLeuValSerLeuLysLysLysLysProPheHisLeuTyrCysValIleTyrIle 44

Qy      104162 --------------CTGATTTGTCTGTAAATCAGTTGAGCCATTACTTCTAGGTGTATA 104206
                             ||||||   |||   :::      |||         :::   :::
Db          45 ProLeuValProLysLeuIleIleLeuPheLeuAspIleAlaPheIleProLysSerLeu 64

Qy      104207 GTTGCTTCTCAAGTTTCCTAAAAACCACCAAGGCAGGCCAGCTACATCCCACTCCTCAAA 104266
               :::   |||||| |||      ||||||                 |||:::|||::::::||
Db          65 Ile---SerGln-PheGlnAsnAsnHisTyrThrHisAsnHisThrAsnHisAsnThrAs 83

Qy      104267 T 104267
               |
Db          83 n 83
```

Search completed: June 27, 2003, 12:16:25
Job time : 39.5 secs